Raw Sequence Listing Error Summary

SERIAL NUMBER: 09/529,342 B

ERROR DETECTED	SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length — Sequence(s)___contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences

8 ___ Skipped Sequences (NEW RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 ___ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220> — Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 00/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003
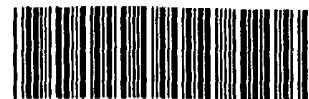
1600

RAW SEQUENCE LISTING   DATE: 06/01/2004
PATENT APPLICATION: US/09/529,342B   TIME: 14:49:54

Input Set : A:\Sequence Listing.asc
Output Set: N:\CRF4\06012004\I529342B.raw

DELETE

W--> 1 1
W--> 3 Error! Main Document Only.
      7 <110> APPLICANT: CLARKE, David John
      8   HARRISON, Michael Henry
      9   AOJULA, Harmesh S.
     11 <120> TITLE OF INVENTION: Particles
     13 <130> FILE REFERENCE: D088026PWO
     15 <140> CURRENT APPLICATION NUMBER: 09/529,342B
     16 <141> CURRENT FILING DATE: 2000-07-27
     18 <150> PRIOR APPLICATION NUMBER: GB9721901.8
     19 <151> PRIOR FILING DATE: 1997-10-16
     21 <160> NUMBER OF SEQ ID NOS: 1
     23 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply
Corrected Diskette Needed
(Pg. 1-2)

ERRORED SEQUENCES

     25 <210> SEQ ID NO: 1
     26 <211> LENGTH: 30
     27 <212> TYPE: PRT
     28 <213> ORGANISM: Artificial Sequence
     30 <220> FEATURE:
     31 <223> OTHER INFORMATION: Description of Artificial Sequence: N,
     32   Myrstic-GALA
     34 <400> SEQUENCE: 1
     35 Trp Glu Ala Ala Leu Ala Glu Ala Leu Ala Glu Ala Leu Ala
E--> 36 Glu His
E--> 37   1   5   10
E--> 38 15
     40 Leu Ala Glu Ala Leu Ala Glu Ala Leu Glu Ala Leu Ala Ala
E--> 41   20   25   30

PLEASE USE ONLY 1 SPACE BETWEE AMINO ACID BASES.

PLEASE SEE ITEM #1 ON ERROR SUMMARY SHEET

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/529,342B

DATE: 06/01/2004
TIME: 14:49:55

Input Set : A:\Sequence Listing.asc
Output Set: N:\CRF4\06012004\I529342B.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:3 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION,
L:36 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:37 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:38 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:41 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1

STATISTICS SUMMARY   DATE: 06/01/2004
PATENT APPLICATION: **US/09/529,342B**   TIME: 14:49:55

Input Set : **A:\Sequence Listing.asc**
Output Set: **N:\CRF4\06012004\I529342B.raw**

Application Serial Number: US/09/529,342B
Alpha or Numeric or Xml: Numeric
Application Class:
Application File Date: 07-27-2000
Art Unit: 1600
Software Application: PatentIN2.0
Total Number of Sequences: 1
Total Nucleotides: 0
Total Amino Acids: 30
Number of Errors: 4
Number of Warnings: 2
Number of Corrections: 0

MESSAGE SUMMARY

259 **W**: 2 (Allowed number of lines exceeded)
332 **E**: 4 ((32) Invalid/Missing Amino Acid Numbering)